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GenCore version 5.1.3
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OM protein - nucleic search, using frame_plus_p2n model

Run on: November 9, 2002, 07:31:31 ; Search time 299 Seconds
(without alignments)
1431.036 Million cell updates/sec

Title: US-09-895-298a-83

Perfect score: 190

Sequence: 1 MANNOPSKAMRASQMMTF.....HDGSLDRSRVSQGNPRA 190

Scoring table:

OLIGO	Xgapop 60.0 , Ygapext 60.0
	Ygapop 60.0 , Ygapext 60.0
	Fgapop 6.0 , Fgapext 7.0
	Delop 6.0 , Delext 7.0

Searched: 2185239 seqs, 112599159 residues

Word size: 4

Total number of hits satisfying chosen parameters: 1316744

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: listing first 45 summaries

Command line parameters:

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-DB=N_Geneseq_101002 -QFMT=fastap -SUFIX=oligna.rng -MINMATCH=0.1 -LOOPL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=oligo -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR.SCORE=quality -THR.MIN=4 -ALIGN=15 -MODE=LOCAL
-OUTFMT=eto -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09895298 -ECGN_1.1.79 -runat_06112002_160752.3557 -NCP=6 -ICU=3
-NO_XLPRX -NO_MAP -LARGEQUERY -NEG.SCORES=0 -WAIT -LONELOG -DEV.TIMEOUT=120
-WARN.TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database :

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- 2: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*
- 3: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:*
- 4: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:*
- 5: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT:*
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- 7: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT:*
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- 10: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT:*
- 11: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT:*
- 12: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT:*
- 13: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT:*
- 14: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:*
- 15: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT:*
- 16: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT:*
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- 19: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:*
- 20: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:*
- 21: /SID2/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:*
- 22: /SID2/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:*
- 23: /SID2/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
- 24: /SID2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	190	100.0	1097	22	ABA08605	Human LAK-4p homol
2	190	100.0	1097	22	AAK53221	Human polynucleoti
3	190	100.0	1219	22	AAF82463	Human CASB6411-rel
4	190	100.0	1312	22	AAK52237	Human polynucleoti
5	190	100.0	1461	21	AAAF8402	Human secreted pro
6	190	100.0	1813	22	AAH18131	Human cDNA sequenc
7	190	100.0	1960	22	AAF82462	Human CASB6411-rel
8	190	100.0	2243	21	AAA64684	cDNA encoding a hu
9	190	100.0	2407	22	AAF82460	Human CASB6411 cDN
10	190	100.0	2521	22	AAF82461	Alternatively spli
11	150	78.9	1194	23	ABV22463	Human prostate exp
12	150	78.9	1194	23	ABV25683	Human prostate exp
13	150	78.9	1194	23	ABV28278	Human prostate exp
14	120	63.2	470	22	AAH18591	Human breast cance
15	110	57.9	501	22	AAH09919	Human breast cance
16	71	37.4	286	23	ABV08852	Human prostate exp
17	71	37.4	617	23	ABV12915	Human prostate exp
18	52	27.4	590	23	ABV34041	Human prostate exp
19	52	27.4	590	23	ABV42908	Human prostate exp
20	50	26.3	777	22	AAH08034	Human cDNA clone (
21	46	24.2	197	22	AAH19767	Human breast cance
22	40	21.1	555	22	AAH20351	Human breast cance
23	35	18.4	454	22	ABAS8847	Human foetal liver
24	35	18.4	454	22	AAK07004	Human brain expres
25	35	18.4	454	22	AAK32745	Human bone marrow
26	35	18.4	454	22	AAH38558	Probe #7244 used t
27	35	18.4	454	22	ABS07543	Human genome-deriv
28	34	17.9	233	22	AAH10187	Human breast cance
29	32	16.8	498	22	AAH11452	Human breast cance
30	31	16.3	94	22	ABAF1379	Human foetal liver
31	31	16.3	94	22	AAK19696	Human brain expres
32	31	16.3	94	22	AAK45716	Human bone marrow
33	31	16.3	94	22	AAH51641	Probe #20327 used
34	31	16.3	94	22	ABH19993	Human genome-deriv
35	29	15.3	523	23	ABV03747	Human prostate exp
36	16	8.4	402	22	AAF65737	Novel human polynu
37	16	8.4	617	22	AAH11030	Human breast cance
38	16	8.4	618	22	AAH18794	Human breast cance
39	12	6.3	775	22	AAH20104	Human breast cance
40	9	4.7	285	16	AAH25867	Human gene signatu
41	9	4.7	330	22	AAH04641	Gene expression pr
42	9	4.7	506	24	ABQ32690	Oligonucleotide fo
43	9	4.7	506	24	ABQ32691	Oligonucleotide fo
44	9	4.7	1391	21	AAH77219	Human OREX ORF2774
45	9	4.7	1399	22	AAH48003	Ribosomal S9 prote

ALIGNMENTS

RESULT 1
ID ABA08605 standard; cDNA; 1097 BP.

ABA08605;

11-JAN-2002 (first entry)

Human LAK-4p homologue-encoding cDNA, SEQ ID NO:381.

Human; cytokine; cell proliferation; cell differentiation; growth factor;
haematopoiesis regulation; tissue growth; immunomodulator; actin;
inhibin; chemotaxis; chemokinesis; thrombolytic; oncogenesis;
proliferation; metastasis; cancer; tumour; haematopoietic disorder;
myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;
chronic inflammatory condition; proliferative retinopathy;
atherosclerosis; coronary heart disease; arterial ischaemia;
bone disorder; osteoporosis; vascular growth disorder;

KW tissue regeneration; wound healing; infection; immune disorder;
KW cell culture; drug screening; gene therapy; antiinflammation;
KW antiasthmatic; antiarthritic; haemostatic; antiatherosclerotic;
KW cytostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial;
KW antifungal; vulnery; antitumor; ss.
XX
OS Homo sapiens.
PN MO200157188-A2.
XX
PD 09-AUG-2001.
XX
PF 05-FEB-2001; 2001MO-US03800.
XX
PR 03-FEB-2000; 2000US-0496914.
XX 27-APR-2000; 2000US-0560875.
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Drmanac RT;
XX
DR WPI: 2001-457740/49.
DR P-PSDB; ABB11361.
XX
XX Human proteins and DNA encoding sequences useful for preventing,
PT treating or ameliorating a medical condition in a mammalian subject
PT e.g. arthritis and cancer -
XX
PS Claim 1; Page 473; 1963pp: English.
XX
CC Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and
CC sequences ABA08225-ABA09574 represent nucleic acids encoding them. The
CC invention also relates to vectors and recombinant host cells comprising a
CC nucleotide of the invention, methods of producing the novel polypeptides,
CC antibodies against the polypeptides, methods of detecting the nucleotides
CC or polypeptides in a sample, and methods of identifying compounds which
CC bind to polypeptides of the invention. Although novel, many of the
CC polypeptides of the invention have homology to known proteins, thereby
CC giving an insight into their probable biological activities, and hence
CC potential therapeutic applications. The polypeptides of the invention may
CC have various activities, including cytokine, cell proliferation or cell
CC differentiation activities; stem cell growth factor activity;
CC haematopoiesis regulatory activity; tissue growth activity;
CC immunomodulatory activity; activin- or inhibin-related activities;
CC chemotactic or chemokinetic activities; haemostatic, thrombotic or
CC thrombolytic activities; receptor or ligand activities; or may be
CC involved in oncogenesis, cancer cell proliferation or metastasis.
CC Depending on their biological activities, polypeptides and nucleotides of
CC the invention are useful for preventing, treating or ameliorating medical
CC conditions, e.g., by protein or gene therapy. Such conditions include
CC cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell
CC disorders), chronic inflammatory conditions (e.g., asthma or arthritis),
CC proliferative retinopathy, atherosclerosis, coronary heart disease,
CC arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal
CC vascular growth. Polypeptides involved with tissue regeneration and
CC repair (or nucleic acids encoding them) may be used to promote wound
CC healing (e.g., of burns, incisions and ulcers), while those with
CC immunomodulatory activities may be used in the treatment of viral,
CC bacterial and fungal infections in addition to immune disorders.
CC Polypeptides with growth factor activity may be used in cell cultures to
CC promote cell growth. For example, such polypeptides may be used to
CC manipulate stem cells in culture to give rise to neuroepithelial cells
CC that can be used to augment or replace cells damaged by illness,
CC autoimmune disease or accidental damage. The polypeptides and nucleotides
CC may also be used in the diagnosis of the above conditions, and in drug
CC screening techniques. The present sequence represents a cDNA encoding a
CC novel human polypeptide of the invention.
XX
SQ Sequence 1097 BP; 288 A; 246 C; 247 G; 316 T; 0 other;

Alignment Scores:

Pred. No.: 2,13e-183
Score: 190.00

Length: 1097
Matches: 190

	Percent Similarity:	100.00%	Conservative:	0
	Best Local Similarity:	100.00%	Mismatches:	0
	Query Match:	100.00%	Indels:	0
	DB:	22	Gaps:	0
US-09-895-298a-83 (1-190) x ABA08605 (1-1097)				
QY 1 MetMetasnpheglnpProposerlysalatrpargalaserglmctettrPhephe	20			
Db 269 ATGATGAATTTCCAGCTCCGAGCAAAAGCCTGGGGGCCCTCAGAGATGACTTTTTC	328			
QY 21 IlePheLeuLeuPhePheProSerPheThrGlyValLeuCysThrLeuAialleThIle	40			
Db 329 ATCTTCTGGCTCTTTTCCATCCTTCACCGGGGGTCTTGACACCCCGGCATCACCATC	388			
QY 41 TrpArgLeuysProserAlaAspCysGlyProPheArgGlyLeuPoleuPheIleHis	60			
Db 389 TGGAGATTGAAGCCTTACGTGACTGTGGCCCTTTTGAGAGTGTGCTCTTCATTAC	448			
QY 61 SerIleTySerTrpIleAspThrIleuSerThrArgProGlyTyTrpValValTrp	80			
Db 449 TCCATCTACAGCTGGATCGACACCCCTAAGTACACGGCCTGCTGCTGGTTGG	508			
QY 81 IleTyArgAsnLeuIleGlySerValHisPhePheIleLeuIleValLeu	100			
Db 509 ATCATCGGAACCTCATGGAAGTGTGCACTTCTTTTCACTCCACCTCATTTGTCTA	568			
QY 101 IleIleThrTyLeuTyrrTPGInIleThrGluGlyArgGlyIleMetIleArgLeuLeu	120			
Db 569 ATCATCACCTTACTTACTGGCAGATCATCAGAGGAAGGAAATGATTAAGGCTGCTC	628			
QY 121 HisGluInIleIleAsnGluGlyLyAspLysMetPheLeuIleGlyLysLeuIleLys	140			
Db 629 CATGACAGATTCATTAATGAGGCAAAAGATTAATGTTCTGTAGTAAATTTGATCAAG	688			
QY 141 LeuGlnAspMetGlyLysLysAlaAsnProSerSerLeuValLeuGluArgGluVal	160			
Db 689 CTGACGATATGTGGAGAAAGCAACCCACGCTCACTTCTTGGAAGAGAGAGTG	748			
QY 161 GluGluInGlyPheLeuHisLeuGlyLysHisAspLysSerLeuAspLeuArgSerArg	180			
Db 749 GAGCAACAAGGCTTTTGGCATTTGGGGGAACATGATGGCAGCTTGACTTGCGATTACA	808			
QY 181 ArgSerValGlnGluGlyAsnProArgAla	190			
Db 809 AGATCACTTCAAGAGGTATTCAGAGGCC	838			
RESULT 2				
AAK53221				
ID AAK53221 standard; cDNA; 1097 BP.				
XX				
AC AAK53221:				
XX				
XX 06-NOV-2001 (first entry)				
DE Human polynucleotide SEQ ID NO 2750.				
XX				
KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;				
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;				
KW tissue growth factor; immunomodulatory; cancer; leukaemia;				
XX nervous system disorder; arthritis; inflammation; ss.				
OS Homo sapiens.				
XX				
PN WO200157190-A2.				
XX				
PD 09-AUG-2001.				
XX				
PF 05-FEB-2001; 2001MO-US04098.				
XX				
PR 03-FEB-2000; 2000US-0496914.				
XX 27-APR-2000; 2000US-0560875.				
PR 20-JUN-2000; 2000US-0598075.				

Score: 190.00 Matches: 190
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 22 Gaps: 0

US-09-895-298a-83 (1-190) x AAF82463 (1-1219)

QY 1 MetMetanPheGlnPropSerLysAlaTrpArgAlaSerGlnMetMetThrPhePhe 20
DB 4 ATGATGAAATTTCCAGCTCCGAGCAAGCCTGGCGGCTCCACAGATGATGACTTTTTC 63
QY 21 IlePheLeuLeuPhePheProSerPheThrGlyValLeuGlyThrLeuAlaIleThrIle 40
DB 64 ATCTTCTGCTCTTTTCCATCTTTCACCGGGGCTTGGACCCCTGGCCATCACCATC 123
QY 41 TrpArgLeuLysProSerAlaAspCysGlyProPheArgLysLeuProLeuPheIleHis 60
DB 124 TGGAGATTGAAGCCTTACGCTGACCTGGCTTTCGAGGCTGCTCTTCATTTCAC 183
QY 61 SerIleTyrSerTrpIleAspThrLeuSerThrArgProGlyTyrLeuTrpValIleTrp 80
DB 184 TCCATCTACAGCTGGATCGACACCCCTAAGTACACGCGCTGCTACCTGGGTTGTTGG 243
QY 81 IleTyrArgAsnLeuIleGlySerValHisPhePheIleLeuThrLeuIleValLeu 100
DB 244 ATCTATCGGAACCTCATCTGGAAGTGTCACTCTTTTTCATCCCTCATTGTTGCTG 303
QY 101 IleIleThrTyrLeuTyrTrpGlnIleThrGlnGlyArgGlyIleMetIleArgLeuLeu 120
DB 304 ATCATCACTTATCTTACTGCGACATCACAGAGGGAAGATTAAGTAAGGCTGCTC 363
QY 121 HisGlnGlnIleLeuAsnGlnGlyLysAspLysMetPheLeuIleGlyLysLeuIleLys 140
DB 364 CATGAGAGAGATCAATTAATGAGGGGGAAGATAAATGTTCTGTAGAGAAAATGATCAAG 423
QY 141 LeuGlnAspMetGlyLysLysAlaAsnProSerSerLeuValLeuGlnArgGlnVal 160
DB 424 CTGCAAGATTTGGAGAAAGCAAAACCCAGCTCTTCTGGAAAGAGAGAGAGTG 483
QY 161 GlnGlnGlnGlyPheLeuHisLeuGlnGlyHisAspGlySerLeuAspLeuArgSerArg 180
DB 484 GAGCAACAAGCTTTTGGCATTTGGGGGAACATGATGGCAGTCTTGACCTTGATCTAGA 543
QY 181 ArgSerValGlnGlnGlyAsnProArgAla 190
DB 544 AGATCACTCAAGAGATTAATCCAAAGGCC 573

RESULT 4
AAK52237
ID AAK52237 standard; cDNA; 1312 BP.
XX
XX AAK52237;
AC AAK52237;
XX
XX 06-NOV-2001 (first entry)
DT
XX
XX Human polynucleotide SEQ ID NO 782.
DE
XX
XX Human: cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorder; arthritis; inflammation; ss.
XX
XX Homo sapiens.
OS
XX
XX WO200157190-A2.
PN
XX
XX 09-AUG-2001.
PD
XX
XX 05-FEB-2001; 2001MO-US04098.
PF
XX
XX 03-FEB-2000; 2000US-0496914.
PR
XX
XX 27-APR-2000; 2000US-0560875.
PR

PR 20-JUN-2000; 2000US-0598075.
PR 19-JUL-2000; 2000US-0620325.
PR 01-SEP-2000; 2000US-0654936.
PR 15-SEP-2000; 2000US-0663561.
PR 20-OCT-2000; 2000US-0693325.
PR 30-NOV-2000; 2000US-0728422.
XX
XX (HYSE-) HYSEQ INC.
PA
XX Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y;
PI Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;
XX WPI: 2001-476283/51.
DR P-SDB; AAM79104.
XX
PT Nucleic acids encoding polypeptides with cytokine-like activities,
PT useful in diagnosis and gene therapy -
XX
PS Claim 1; Page 2615-2616; 6221pp; English.
PS
XX The invention relates to polynucleotides (AAK51456-AAK53435) and the
CC encoded polypeptides (AAM78323-AAK80302) that exhibit activity elating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation.
CC Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666
CC (AAM80020) are omitted as the relevant pages from the sequence listing
CC were missing at the time of publication.
XX
SQ Sequence 1312 BP; 370 A; 286 C; 287 G; 369 T; 0 other;

Alignment Scores:
Pred. No.: 2,53e-183 Length: 1312
Score: 190.00 Matches: 190
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 22 Gaps: 0

US-09-895-298a-83 (1-190) x AAK52237 (1-1312)

QY 1 MetMetanPheGlnPropSerLysAlaTrpArgAlaSerGlnMetMetThrPhePhe 20
DB 294 ATGATGAAATTTCCAGCTCCGAGCAAGCCTGGCGGCTCCACAGATGATGACTTTTTC 353
QY 21 IlePheLeuLeuPhePheProSerPheThrGlyValLeuGlyThrLeuAlaIleThrIle 40
DB 354 ATCTTCTGCTCTTTTCCATCTTTCACCGGGGCTTGGACCCCTGGCCATCACCATC 413
QY 41 TrpArgLeuLysProSerAlaAspCysGlyProPheArgLysLeuProLeuPheIleHis 60
DB 414 TGGAGATTGAAGCCTTACGCTGACCTGGCTTTCGAGGCTGCTCTTCATTTCAC 473
QY 61 SerIleTyrSerTrpIleAspThrLeuSerThrArgProGlyTyrLeuTrpValIleTrp 80
DB 474 TCCATCTACAGCTGGATCGACACCCCTAAGTACACGCGCTGCTACCTGTTGGTTTGG 533
QY 81 IleTyrArgAsnLeuIleGlySerValHisPhePheIleLeuThrLeuIleValLeu 100
DB 534 ATCTATCGGAACCTCATCTGGAAGTGTGACCTTTTTCATCCCTCACCCTCATTTGCTGA 593
QY 101 IleIleThrTyrLeuTyrTrpGlnIleThrGlnGlyArgGlyIleMetIleArgLeuLeu 120
DB 594 ATCATCACTTATCTTACTGCGACATCACAGAGGGAAGATTAAGTAAGGCTGCTC 653
QY 121 HisGlnGlnIleLeuAsnGlnGlyLysAspLysMetPheLeuIleGlyLysLeuIleLys 140

```
Db 654 CATGAGCAGATCATTAATGAGGGCAAGATAAATGTTCTGATGAAAAATGATCAAG 713
QY 141 LeuGlnAspMetGluLysLysAlaAsnProSerSerLeuValLeuGluArgArgLysVal 160
Db 714 CTGCGAGATATGGAAGAAGCAAGCCAGCTCATTGTTCTGAAAGGAGAGGGT 773
QY 161 GluGlnGlnGlyPheLeuHisLeuGlyGluHisAspGlySerLeuAspLeuArgSerArg 180
Db 774 GAGCAACAAGGCTTTTTCATTGGGGGACATGATGACGCTTGACTTGGCATCTAGA 833
QY 181 ArgSerValGlnGlnGlyAsnProArgAla 190
Db 834 AGATCAGTTCAAGAGGTAAATCCAGGGCC 863

RESULT 5
AAH78402
ID AAA78402 standard; cDNA; 1461 BP.
XX
XX AAA78402;
AC
XX
XX 20-NOV-2000 (first entry)
DE
XX Human secreted protein gene 22 SEQ ID NO:32.
XX
XX Human; secreted protein; cytostatic; antianaemic; antidiabetic;
XX antiinflammatory; ophthalmological; antirheumatic; antiarthritic;
XX antipruritic; antiangiogenic; cardiant; anti-HIV; nootropic;
XX neuroprotective; antimicrobial; antiparkinsonian; cancer;
XX immune system disorder; angiogenesis; hyperproliferative disorder;
XX cardiovascular disorder; apoptosis; neurological disease;
XX infectious disease; wound healing; ss.
XX
XX Homo sapiens.
XX
XX WO200035937-A1.
XX
XX 22-JUN-2000.
XX
XX 16-DEC-1999; 99WO-US29950.
XX
XX 17-DEC-1998; 98US-0112809.
XX
XX 18-DEC-1998; 98US-0113006.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Ruben SM, Ebner R, Rosen CA, Endress GA, Soppet DR, Ni J,
XX Duan DR, Moore PA, Shi Y, Lafleur DW, Olsen HS, Florence K;
XX
XX MPI; 2000-431566/37.
XX
XX P-PSDB; AAB24458.
XX
XX Forty seven human nucleic acids encoding secreted proteins, useful in
XX the treatment, prevention and diagnosis of cancers, disorders of the
XX immune system, angiogenesis disorders, neurological diseases and
XX hyperproliferative disorders -
XX
XX Claim 1; Page 457-458; 562pp; English.
XX
XX The polynucleotide sequence given in AAA78381 to AAA78432 encode the
XX human secreted proteins given in AAB24437 to AAB24604. Human secreted
XX proteins have activities based on the tissues and cells the genes are
XX expressed in. Examples of activities includes: cytostatic; antianaemic;
XX antidiabetic; antiinflammatory; ophthalmological; antirheumatic;
XX antiarthritic; antipruritic; antiangiogenic; cardiant; anti-HIV;
XX nootropic; neuroprotective; antimicrobial and antiparkinsonian.
XX Human secreted protein polynucleotides, polypeptides, antagonists and/or
XX agonists may be useful in treating, preventing, and/or diagnosing other
XX diseases, disorders, and/or conditions such as: (a) cancers; (b)
XX disorders of the immune system; (c) angiogenesis disorders; (d)
XX hyperproliferative disorders; (e) cardiovascular disorders; (f) diseases
XX associated with increase apoptosis; (g) neurological diseases; and
XX (h) infectious diseases. They are also used to promote wound healing.
```

```
CC AAA78372 to AAA78380 and AAB24436 represent sequences used in the
CC exemplification of the present invention.
XX
SQ Sequence 1461 BP; 428 A; 312 C; 324 G; 397 T; 0 other;

Alignment Scores:
Pred. No.: 2,81e-183 Length: 1461
Score: 190.00 Matches: 190
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 21 Gaps: 0

US-09-895-298a-83 (1-190) x AAA78402 (1-1461)
QY 1 MetMetAsnPheGlnProProSerLysAlaTrpArgAlaSerGlnMetMetThrPhePhe 20
Db 63 ATGATGAATTTCCACCTCCGAGCAAGCGTGGCGGCTCCACAGATGATGACTTTCTTC 122
QY 21 IlePheLeuLeuPhePheProSerPheThrGlyValLeuCysThrLeuAlaIleThrIle 40
Db 123 ATCTTCTTGCTTTTTCATCTTTCACCGGGGCTTGTGACACCTGGCCATCCATC 182
QY 41 TrpArgLeuLysProSerAlaAspCysGlyProPheArgGlyLeuProLeuPheIleHis 60
Db 183 TGGAGATTGAACCTTCAAGCTGACGTGGCCCTTTTCAGAGTCTGCTCTTCATTCAC 242
QY 61 SerIleTySerTrpIleAspThrLeuSerThrArgProGlyTyTrpLeuTrpValTrp 80
Db 243 TCCATCTACAGCTGGATGCACACCTTAAGTACACGGCCCTGACTGTGGCTTGTGG 302
QY 81 IleTyArgAsnLeuIleGlySerValHisPhePheIleLeuThrLeuIleValLeu 100
Db 303 ATCTATCGGAACCTCATTTGGAAGTGTGACCTTTTTCATCTACCTCATTTGTCTA 362
QY 101 IleIleThrTyLeuTyTrpGlnIleThrGlnGlyArgLysIleMetIleArgLeuLeu 120
Db 363 ATCATCACCCTATCTTTACTGCGAGATCACAGAGGAGCAAGATATATGTAAGGCTGCTC 422
QY 121 HisGlnGlnIleIleAsnGlnGlyLysAspLysMetPheLeuIleGluLysLeuIleLys 140
Db 423 CATGAGCAGATCATTAATGAGGGCAAGAGATAAAGTTCCTATGAAAAATTGATCAAG 482
QY 141 LeuGlnAspMetGluLysLysAlaAsnProSerSerLeuValLeuGluArgArgLysVal 160
Db 483 CTGCAAGATATGAGAGAGAAACCAACCCACCTCATTGTTCTGGAAGGAGAGAGGTG 542
QY 161 GluGlnGlnGlyPheLeuHisLeuGlyGluHisAspGlySerLeuAspLeuArgSerArg 180
Db 543 GAGCAACAAGGCTTTTTCATTGGGGGAAACATGATGCGACGCTTGACTTGGCATCTAGA 602
QY 181 ArgSerValGlnGlnGlyAsnProArgAla 190
Db 603 AGATCAGTTCAAGAGGTAAATCCAGGGCC 632

RESULT 6
AAH18131
ID AAH18131 standard; cDNA; 1813 BP.
XX
XX AAH18131;
AC
XX 26-JUN-2001 (first entry)
DE
XX Human cDNA sequence SEQ ID NO:18001.
XX
XX Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
XX Homo sapiens.
XX
XX EP1074617-A2.
XX
XX 07-FEB-2001.
XX
```

PF 28-JUL-2000; 2000EP-0116126.
 XX
 PR 29-JUL-1999; 99JP-0248036.
 PR 27-AUG-1999; 99JP-0300253.
 PR 11-JAN-2000; 2000JP-0118776.
 PR 02-MAY-2000; 2000JP-0183767.
 PR 09-JUN-2000; 2000JP-0241899.
 XX
 PA (HELI-) HELIX RES INST.
 PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
 PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
 DR WPI; 2001-318749/34.
 XX
 PT Primer sets for synthesizing polynucleotides, particularly the 5602
 PT full-length cDNAs defined in the specification, and for the detection
 PT and/or diagnosis of the abnormality of the proteins encoded by the
 PT full-length cDNAs -
 XX
 PS Claim 8; SEQ ID 18001; 2537pp + CD ROM; English.
 XX
 CC The present invention describes primer sets for synthesizing 5602
 CC full-length cDNAs defined in the specification. Where a primer set
 CC comprises: (a) an oligo-dT primer and an oligonucleotide complementary
 CC to the complementary strand of a polynucleotide which comprises one of
 CC the 5602 nucleotide sequences defined in the specification, where the
 CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
 CC of an oligonucleotide comprising a sequence complementary to the
 CC complementary strand of a polynucleotide which comprises a 5'-end
 CC sequence and an oligonucleotide comprising a sequence complementary to a
 CC polynucleotide which comprises a 3'-end sequence, where the
 CC oligonucleotide comprises at least 15 nucleotides and the combination of
 CC the 5'-end sequence/3'-end sequence is selected from those defined in
 CC the specification. The primer sets can be used in antisense therapy and
 CC in gene therapy. The primers are useful for synthesizing polynucleotides,
 CC particularly full-length cDNAs. The primers are also useful for the
 CC detection and/or diagnosis of the abnormality of the proteins encoded by
 CC the full-length cDNAs. The primers allow obtaining of the full-length
 CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
 CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to
 CC AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632
 CC represent oligonucleotides, all of which are used in the exemplification
 CC of the present invention.
 CC
 XX
 SQ Sequence 1813 BP; 489 A; 400 C; 405 G; 519 T; 0 other;
 XX
 Alignment Scores:
 Pred. No.: 3,46e-183 Length: 1813
 Score: 190.00 Matches: 190
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 22 Gaps: 0
 US-09-895-298a-83 (1-190) x AAH18131 (1-1813)
 QY 1 MetMetasAnpHeGlnProProSerLyAlaTrpArgAlaSerGlnMetMetThrPhePhe 20
 DB 451 ATGATGAAATTTCCAGCTCCGAGCAAGGCTGCGGCGCTCACAGATGATGACTTTCTTC 510
 QY 21 IlePheLeuLeuPhePheProSerPheThrGlyValLeuGlyThrLeuAlaIleThrIle 40
 DB 511 ATCTTCTGCTCTTTTCCATCCTTCACCGGGGTCTTGACACCCCTGGCCATCACCATC 570
 QY 41 TrpArgLeuLysProSerAlaAspCysGlyProPheArgGlyLeuProLeuPheIleHis 60
 DB 571 TGGAGATGTAAGCCCTTCAGCTGAGCTGGCCCTTTTCGAGAGTCTGCTCTTCATTCAC 630
 QY 61 SerIleTyrSerTrpIleAspThrLeuSerThrArgProGlyTyrLeuTrpValValTrp 80
 DB 631 TCCATCTACAGCTGATGACACCCCTTAAGTACACGGGCTGCTACCTGCTGCTTGG 690

QY 81 IleTyrArgAsnLeuIleGlySerValHisPhePheIleLeuThrLeuIleValLeu 100
 DB 691 ATCATCGAAGCTCATTTGAAAGTGTCACTCTTTTTCATCCCAACCTCATTTGCTCTA 750
 QY 101 IleIleThrTyrLeuTyrTrpGlnIleThrGlnGlyArgGlyIleMetIleArgLeuLeu 120
 DB 751 ATCATCAGCTTATCTTTTACTGTCGACATCACAGAGGAAGAGATTATGATTAAGGCTCTC 810
 QY 121 HisGlnGlnIleIleAsnGlnGlyLysAspLysMetPheLeuIleGlyLysLeuIleLys 140
 DB 811 CATGAGACAGATCATTTATGAGGCGCAAGATTAATGTTCTGTATAGAAAATGATCAAG 870
 QY 141 LeuGlnAspMetGluLysLysAlaAsnProSerSerLeuValLeuGluArgGluVal 160
 DB 871 CTCAGAGATATGAGAAAGAAAGCAACCCAGCTCATCTTCTGCAAAAGAGAGAGCTG 930
 QY 161 GlnGlnGlnIlePheLeuHisLeuGlyGlnHisAspGlySerLeuAspLeuArgSerArg 180
 DB 931 GAGCAACAGAGCTTTTGGCATTTGGGGGAAACATGATGACGCTTGACTTGACATCTAGA 990
 QY 181 ArgSerValGlnGlnGlyAsnProArgAla 190
 DB 991 AGATCAGTTCAAGAGATATCCAGAGGCC 1020
 RESULT 7
 AAF82462
 ID AAF82462 standard; cDNA; 1960 BP.
 XX
 AC AAF82462:
 XX
 DT 29-JUN-2001 (first entry)
 XX
 DE Human CASB6411-related cDNA #1.
 XX
 KW Human: CASB6411; vaccine; gene therapy; immunoprophylaxis;
 KW ovarian cancer; colon cancer; autoimmune disease; SS.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..1317
 FT /tag= a
 FT /partial
 FT /note= "this sequence does not contain a start codon"
 XX
 PN MO200123417-A2.
 XX
 PD 05-APR-2001.
 XX
 PF 27-SEP-2000; 2000MO-EP09500.
 XX
 PR 30-SEP-1999; 99GB-0023154.
 PR 07-JUL-2000; 2000GB-0016839.
 XX
 PA (SMK) SMITHKLINE BEECHAM BIOLOGICALS.
 XX
 PI Vlnals De Bassols YC;
 PI
 DR WPI: 2001-316133/33.
 DR P-PSDB: AAB83081.
 XX
 PT Novel CASB6411 polypeptides useful in diagnostics, and as vaccines for
 PT prophylactic and therapeutic treatment of cancers, particularly ovarian
 PT and colon cancers, autoimmune diseases and related conditions -
 XX
 PS Claim 32; Page 65-66; 95pp; English.
 XX
 CC The present sequence is provided in a specification relating
 CC to CASB6411 polypeptides comprising a sequence having at least 70%
 CC identity to a sequence of 460 or 154 amino acids fully defined in
 CC the specification. CASB6411 polypeptides and polynucleotides are
 CC useful for treating a subject by immunoprophylaxis or therapy.
 CC The CASB6411 polypeptides are useful in diagnostics, and as

CC vaccines for prophylactic and therapeutic treatment of cancers,
 CC particularly ovarian and colon cancers, autoimmune diseases and related
 CC conditions. CASB6411 polypeptides are also useful for the
 CC structure-based design of agonists, antagonists or inhibitors of the
 CC polypeptide.

XX SQ Sequence 1960 BP; 515 A; 439 C; 447 G; 559 T; 0 other;

Alignment Scores:

Pred. No.: 3.73e-183 Length: 1960
 Score: 190.00 Matches: 190
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 22 Gaps: 0

US-09-895-298a-83 (1-190) x AAF82462 (1-1960)

OY 1 MetMetAsnPhgGlnProProSerLysAlaTrpArgAlaSerGlnMetMetThrPhePhe 20
 DB 745 ATGATGAAATTCACGCTCCGAGCAAGCTGGCGGCTCCACAGATGACTTTCTTC 804
 OY 21 IlePheLeuLeuPhePheProSerPheThrGlyValLeuGlyThrLeuAlaIleThrIle 40
 DB 805 ATCTTCTGCTCTTTTCCCATCTTTCACCGGGGCTGTGGCACCCTGGCCATCAACATC 864
 OY 41 TrpArgLeuLysProSerAlaAspCysGlyProPheArgGlyLeuProLeuPheIleHis 60
 DB 865 TGGAAATTCGAACCTTCAGCTGACTGTGGCCCTTTTCGAGGCTCCCTCTTCATTCAC 924
 OY 61 SerIleYrSerTrpIleAspThrLeuSerThrArgProGlyTrpLeuTrpValValTrp 80
 DB 925 TCCATCTACAGCTGATGACACCTTAAGTACACGCGCTGACTGTGGGTTGTTGG 984
 OY 81 IleYrArgAsnLeuIleGlySerValHisPhePheIleLeuThrLeuIleValLeu 100
 DB 985 ATCTATCGGAACCTCATTTGGAAGTGTGCACTTCTTTTCATCTCACCCTCATTTGGCTG 1044
 OY 101 IleIleThrTrpLeuTrpTrpGlnIleThrGlnGlyArgGlyIleMetIleArgLeuLeu 120
 DB 1045 ATCATCACCCTATCTTACTCGGAGATCACAGAGGAGAAAGATTAATGTAAGGCTGCTC 1104
 OY 121 HisGlnGlnIleIleAsnGlnGlyLysAspLysMetPheLeuIleGlnLysLeuIleLys 140
 DB 1105 CATGAGCAGATCATTAATGAGGCAAGATTAATGTTCTCTATGAAAAAATTGATCAAG 1164
 OY 141 LeuGlnAspMetGlnLysLysAlaAsnProSerSerLeuValLeuGlnLuarArgGlnVal 160
 DB 1165 CTGCAAGATATGAGAAAGAAAGCAAAACCCACCTCCTGTTCTGTGAAGAGAGAGGTG 1224
 OY 161 GlnGlnGlnGlnGlyPheLeuHisLeuGlnHisAspGlySerLeuAspLeuArgSerArg 180
 DB 1225 GAGCAACCAAGGCTTTTGGATTGGGGCAACATGATGAGTCTGACTTGGCATCTAGA 1284
 OY 181 ArgSerValGlnGlnGlyAsnProArgAla 190
 DB 1285 AGATCAGTTCAAGAGGTAATCCAAAGGCC 1314

RESULT 8
 AAA64684
 ID AAA64684 standard; cDNA; 2243 BP.
 AC AAA64684;
 XX 02-JAN-2001 (first entry)
 DE CDNA encoding a human leukocyte and blood related protein (LBAP).
 XX
 KW Human; leukocyte and blood related protein; LBAP; arteriosclerosis;
 KW cell proliferative disorder; actinic keratosis; atherosclerosis;
 KW bursitis; cirrhosis; hepatitis; mixed connective tissue disease; MCTD;
 KW myelofibrosis; paroxysmal nocturnal hemoglobinuria; cancer;
 KW adenocarcinoma; leukemia; lymphoma; melanoma; sarcoma;

KW teratocarcinoma; autoimmune disorder; inflammatory disorder;
 KW acquired immunodeficiency syndrome; AIDS; Addison's disease;
 KW adult respiratory distress syndrome; allergy; ankylosing spondylitis;
 KW amyloidosis; anaemia; asthma; autoimmune haemolytic anaemia; infection;
 KW Werner syndrome; haemodialysis; extracorporeal circulation; trauma; ss.
 XX
 OS Homo sapiens.

PH Key Location/Qualifiers
 FT CDS 109..1272
 FT sig_peptide /product= "Leukocyte and blood related protein (LBAP)"
 FT 109..261
 FT /*tag= b

XX WO200052161-A2.

XX 08-SEP-2000.

XX 29-FEB-2000; 2000WO-US05153.

XX 01-MAR-1999; 99US-0122080.

XX (INCY-) INCYTE PHARM INC.

PI Lal P, Yue H, Hillman JL, Lu DAM, Baughn MR, Tang YT, Azimzal Y;

DR WPI; 2000-587310/55.

DR P-PSDB; AAB08764.

PT Leukocyte and blood associated proteins and polynucleotides encoding
 PT them, useful for diagnosis, treatment and prevention of
 PT autoimmune/inflammatory disorders and cell proliferative disorders
 PT including cancer -

XX Claim 4; Page 68-69; 70pp; English.

CC The present sequence encodes a human leukocyte and blood related
 CC protein, designated LBAP. LBAP polynucleotides and polypeptides are
 CC useful for treating or preventing a disorder associated with decreased
 CC expression or activity of LBAP including a cell proliferative disorder
 CC such as actinic keratosis, arteriosclerosis, atherosclerosis, bursitis,
 CC cirrhosis, hepatitis, mixed connective tissue disease (MCTD),
 CC myelofibrosis, paroxysmal nocturnal hemoglobinuria, etc., cancers
 CC including adenocarcinoma, leukemia, lymphoma, melanoma, myeloma,
 CC sarcoma, teratocarcinoma and in particular cancers of the adrenal
 CC gland, bladder, bone, bone marrow, brain, breast, cervix, etc., and
 CC an autoimmune/inflammatory disorder such as acquired immunodeficiency
 CC syndrome (AIDS), Addison's disease, adult respiratory distress syndrome,
 CC allergies, ankylosing spondylitis, amyloidosis, anaemia, asthma,
 CC atherosclerosis, autoimmune haemolytic anaemia, etc., Werner syndrome,
 CC complications of cancer, haemodialysis, and extracorporeal circulation,
 CC viral, bacterial, fungal, parasitic, protozoan, and helminthic
 CC infections, and trauma.

XX SQ Sequence 2243 BP; 602 A; 500 C; 520 G; 621 T; 0 other;

Alignment Scores:

Pred. No.: 4.25e-183 Length: 2243
 Score: 190.00 Matches: 190
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 21 Gaps: 0

US-09-895-298a-83 (1-190) x AAA64684 (1-2243)

OY 1 MetMetAsnPhgGlnProProSerLysAlaTrpArgAlaSerGlnMetMetThrPhePhe 20
 DB 700 ATGATGAAATTCACGCTCCGAGCAAGCTGGCGGCTCCACAGTATGACTTTCTTC 759
 OY 21 IlePheLeuLeuPhePheProSerPheThrGlyValLeuGlyThrLeuAlaIleThrIle 40
 DB 805 ATCTTCTGCTCTTTTCCCATCTTTCACCGGGGCTGTGGCACCCTGGCCATCAACATC 864

```
Db 760 ATCTCTGCTCTTTTCCCATCTTCACCGGGGCTTTGGACCCCTGGCCATCCACCATC 819
Qy 41 TTPArgLeuLysProSerAlaAspCysGlyProPheArgGlyLeuProLeuPheIleHis 60
Db 820 TGGAGATTGAAGCCTTCAGCTGAGTGGCCCTTTTCAGAGTCCGCTCTTCATTCAC 879
Qy 61 SerIleThrTyrlleuTyrlleuSerThrArgProGlyTyrlleuTyrlleuValTrp 80
Db 880 TCCATCTACAGCTGGAGACACCCCTAAGTACACGGGCTGGTACCTGGTGGTTGG 939
Qy 81 ILTYrArgSnlleuIleGlySerValHisPhePheIleuThrIleuValleu 100
Db 940 ATCTATCGAAGCTCATTTGGAAGTGTCACTTCTTTTCATCTCCACCTCATTTGCTTA 999
Qy 101 ILleIleThrTyrlleuTyrlleuTrpGlnIleThrGluGlyArgLysIleMetIleArgLeu 120
Db 1000 ATCATCACTATCTTACTGTCGAGATCACAGAGGAAGAAATTATGATTAAGGCTGCTC 1059
Qy 121 HisGluGlnIleIleAsnGluGlyLysAspLysMetPheLeuIleGlyLysLeuIleLys 140
Db 1060 CATGAGCAGATTCATTAATGAGGGCCAAAGATMAATGTTCTGTAGAAAATTGATCAAG 1119
Qy 141 LeuGlnAspMetGluLysLysAlaAsnProSerSerIleuValleuGluArgArgGluVal 160
Db 1120 CTCGAGGATATGAGAGAAAGCAACCCAGCTCATCTTCTCGAAGAGAGAGAGTG 1179
Qy 161 GluGlnGlnGlyPheLeuHisLeuGlyGluHisAspGlySerLeuAspLeuArgSerArg 180
Db 1180 GAGCAACAAGGCTTTTGGCATTTGGGGGCAACATGAGCGAGTGTGACTTGCGCATCTAGA 1239
Qy 181 ArgSerValGlnGluGlyAsnProArgAla 190
Db 1240 AGATCAGTTCAAGAGATATCCAGGGCC 1269
RESULT 9
AAf82460
ID AAF82460 standard; cDNA; 2407 BP.
AC AAF82460;
XX 29-JUN-2001 (first entry)
DE Human CASB6411 cDNA.
XX Human; CASB6411; vaccine; gene therapy; immunoprophylaxis;
KM ovarian cancer; colon cancer; autoimmune disease; ss.
XX Homo sapiens.
OS
FH key Location/Qualifiers
FT CDS 382..1764
FT /tag= a
FT /product= "CASB6411"
XX
XX WO200123417-A2.
XX
XX 05-APR-2001.
XX
XX 27-SEP-2000; 2000MO-EP09500.
XX
XX 30-SEP-1999; 99GB-0023154.
XX 07-JUL-2000; 2000GB-0016839.
XX
XX (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
XX
XX Vinals De Baselos YC;
XX
XX WPI; 2001-316133/33.
XX
XX P-PSDB; AAB83079.
XX
XX Novel CASB6411 polypeptides useful in diagnostics, and as vaccines for
PT prophylactic and therapeutic treatment of cancers, particularly ovarian
PT and colon cancers, autoimmune diseases and related conditions -
```

```
XX
PS Claim 11: Page 63-64; 95pp; English.
XX
CC The present sequence encodes human CASB6411 polypeptide. The
CC invention relates to CASB6411 polypeptides comprising a sequence
CC having at least 70% identity to a sequence of 460 or 154 amino acids
CC fully defined in the specification. CASB6411 polypeptides and
CC polynucleotides are useful for treating a subject by immunoprophylaxis
CC or therapy. The CASB6411 polypeptides are useful in diagnostics, and
CC as vaccines for prophylactic and therapeutic treatment of cancers,
CC particularly ovarian and colon cancer, autoimmune diseases and related
CC conditions. CASB6411 polypeptides are also useful for the
CC structure-based design of agonists, antagonists or inhibitors of the
CC polypeptide. The present sequence may be alternatively spliced to
CC generate a sequence encoding a truncated CASB6411 protein.
XX
SQ Sequence 2407 BP; 635 A; 557 C; 546 G; 669 T; 0 other:
Alignment Scores:
Pred. No.: 4,55e-183 Length: 2407
Score: 190.00 Matches: 190
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 22 Gaps: 0
US-09-895-298a-83 (1-190) x AAF82460 (1-2407)
Qy 1 MetMetAspMetGlnProProSerLysAlaTrpArgAlaSerGlnMetMetThrPhePhe 20
Db 1192 ATGATGAATTTCCAGCTCCGAGCAAGCCCTGGGGCCCTCACAGATGAGACTTTCTTC 1251
Qy 21 ILPheLeuLeuPhePheProSerPheThrGlyValLeuGlyThrLeuAlaIleThrIle 40
Db 1252 ATCTTCTGCTCTTTTCCCATCTTCACCGGGGTCTTGCGACCCGCGCATCCACATC 1311
Qy 41 TTPArgLeuLysProSerAlaAspCysGlyProPheArgGlyLeuProLeuPheIleHis 60
Db 1312 TGGAGATTGAAGCCTTCAGCTGAGTGGCCCTTTTGAAGTCTGCTCTTCATTCAC 1371
Qy 61 SerIleThrTyrlleuTyrlleuSerThrArgProGlyTyrlleuTyrlleuValTrp 80
Db 1372 TCCATCTACAGCTGGAGTGCACACCTTAAGTACAGGGCTGGTCACTGTGGTTGG 1431
Qy 81 ILTYrArgSnlleuIleGlySerValHisPhePheIleuThrIleuValleu 100
Db 1432 ATCTATCGAAGCTCATTTGGAAGTGTCACTTCTTTTCATCTCCACCTCATTTGCTTA 1491
Qy 101 ILleIleThrTyrlleuTyrlleuTrpGlnIleThrGluGlyArgLysIleMetIleArgLeu 120
Db 1492 ATCATCACTATCTTACTGTCGAGATCACAGAGGAAGAAATTATGATTAAGGCTGCTC 1551
Qy 121 HisGluGlnIleIleAsnGluGlyLysAspLysMetPheLeuIleGlyLysLeuIleLys 140
Db 1552 CATGAGCAGATTCATTAATGAGGGCAAGATMAATGTTCTGTAGAAAATTGATCAAG 1611
Qy 141 LeuGlnAspMetGluLysLysAlaAsnProSerSerIleuValleuGluArgArgGluVal 160
Db 1612 CTCGAGGATATGAGAGAAAGCAACCCAGCTCATCTTCTTGGAAGAGAGAGGTG 1671
Qy 161 GluGlnGlnGlyPheLeuHisLeuGlyGluHisAspGlySerLeuAspLeuArgSerArg 180
Db 1672 GAGCAACAAGGCTTTTGGCATTTGGGGGCAACATGAGCGAGTGTGACTTGCATCTAGA 1731
Qy 181 ArgSerValGlnGluGlyAsnProArgAla 190
Db 1732 AGATCAGTTCAAGAGATATCCAGGGCC 1761
RESULT 10
AAf82461
ID AAF82461 standard; cDNA; 2521 BP.
XX
XX AAF82461;
```

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XX 29-JUN-2001 (first entry)
DE Alternatively spliced human CASB6411 cDNA encoding truncated protein.
XX
XX Human; CASB6411; vaccine; gene therapy; immunoprophylaxis;
XX ovarian cancer; colon cancer; autoimmune disease; isoform;
XX alternative splicing; ss.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 382..846
XX /*tag= a
XX /product= "truncated CASB6411"
XX
XX WO200123417-A2.
XX
XX 05-APR-2001.
XX
XX 27-SEP-2000; 2000WO-EP09500.
XX
XX 30-SEP-1999; 99GB-0023154.
XX 07-JUL-2000; 2000GB-0016839.
XX
XX (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
XX
XX Vinals De Bassols YC;
XX WPI; 2001-316133/33.
XX P-PSDB; AAB83080.
XX
XX Novel CASB6411 polypeptides useful in diagnostics, and as vaccines for
XX prophylactic and therapeutic treatment of cancers, particularly ovarian
XX and colon cancers, autoimmune diseases and related conditions -
XX
XX Claim 11; Page 64-65; 95pp; English.
XX
XX The present sequence encodes a truncated CASB6411 polypeptide. It
XX is generated by alternative splicing of the full length human cDNA
XX sequence of CASB6411. The invention relates to CASB6411 polypeptides
XX comprising a sequence having at least 70% identity to a sequence of
XX 460 or 154 amino acids fully defined in the specification. CASB6411
XX polypeptides and polynucleotides are useful for treating a subject by
XX immunoprophylaxis or therapy. The CASB6411 polypeptides are useful in
XX diagnostics, and as vaccines for prophylactic and therapeutic treatment
XX of cancers, particularly ovarian and colon cancers, autoimmune diseases
XX and related conditions. CASB6411 polypeptides are also useful for the
XX structure-based design of agonists, antagonists or inhibitors of the
XX polypeptide.
XX
XX SQ Sequence 2521 BP; 662 A; 583 C; 583 G; 693 T; 0 other;
XX
XX Alignment Scores:
XX Pred. No.: 4,76e-183 Length: 2521
XX Score: 190.00 Matches: 190
XX Percent Similarity: 100.00% Conservative: 0
XX Best Local Similarity: 100.00% Mismatches: 0
XX Query Match: 100.00% Indels: 0
XX DB: 22 Gaps: 0
XX
XX US-09-895-298a-83 (1-190) x AAF82461 (1-2521)
XX
XX 1 MetMetAsnPhgGlnProFroSerLysAlaTrpArgAlaSerGlnMetThrPhePhe 20
XX |
XX DB 1306 ARGATGAATTCACAGCTCCGAGCAAAAGCGCTGCGGCGCTCACAGATGATGACTTCTTC 1365
XX |
XX QY 21 IlePheLeuLeuPhePheProSerPheThrGlyValLeuGlyThrLeuAlaIleThrIle 40
XX |
XX DB 1366 ATCTTCTTCCTCTTTTCCCATCTTCACCGGGGCTTGTGACACCTGCGCATCACCATC 1425
XX |
XX QY 41 TrpArgLeuLeuProSerAlaAspCysGlyProPheArgGlyLeuProLeuPheIleHis 60
XX |
|
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```
DB 1426 TGGAGATTGAAGCCTTCACGCTGACTGTGGCCCTTTTCGAGGTCTGCTCTTCATTCAC 1485
QY 61 SerIleTyrSerTrpIleAspThrLeuSerThrArgProGlyTyrLeuTrpValValTrp 80
DB 1486 TCCATCTACAGCTGGATGACACCCCTAAGTACACGCGCTGCTACCTGTGGTGTGGTGG 1545
QY 81 IleTyrAsnLeuIleGlySerValHisPhePheIleLeuThrLeuIleValLeu 100
DB 1546 ATCTATCGGACCTTCATTGGAGAGTGTGCATCTTTTCATCTCCTACCTCATTTGTGCTA 1605
QY 101 IleIleThrTyrLeuTyrTrpGlnIleThrGlnGlyArgGlyIleMetIleArgLeuLeu 120
DB 1606 ATCATCACCCTATCTTACTGCGAGATCACAGAGGAGAGATATATGATTAAGCTGCTGC 1665
QY 121 HisGlnGlnIleIleAsnGlnGlyLysAspLysMetPheLeuIleGlyLysLeuIleLys 140
DB 1666 CATGAGCAGATCATTAATGAGGCGCAAGATAAAGTTCTGATGAAAAATGTATCAAG 1725
QY 141 LeuGlnAspMetGlyLysLysAlaAsnProSerSerLeuValLeuGlnArgGluVal 160
DB 1726 CTGACGATATGAGAGAGAACCAACCCAGCTCCTGTTCTTGGAAGAGAGAGGTG 1785
QY 161 GluGlnGlnGlyPheLeuHisLeuGlyGlnHisAspGlySerLeuAspLeuArgSerArg 180
DB 1786 GAGCAACAAGGCTTTTGGATTTGGGGGAAACATGATGGCAGTCTGACTTGGCATCTAGA 1845
QY 181 ArgSerValGlnGlnGlyAsnProArgAla 190
DB 1846 AGATCAGTTCAGAAAGATATCAAGGCGC 1875
XX
XX RESULT 11
XX ID ABV22463 standard; cDNA; 1194 BP.
XX AC ABV22463;
XX DT 13-SEP-2002 (first entry)
XX
XX Human prostate expression marker cDNA 22454.
XX
XX Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
XX pharmacogenomic marker; gene; ss.
XX
XX Homo sapiens.
XX
XX WO200160860-A2.
XX
XX 23-AUG-2001.
XX
XX 20-FEB-2001; 2001WO-US05171.
XX
XX 17-FEB-2000; 2000US-183319P.
XX 16-MAR-2000; 2000US-189862P.
XX 25-MAY-2000; 2000US-207454P.
XX 09-JUN-2000; 2000US-211314P.
XX 18-JUL-2000; 2000US-219007P.
XX 13-DEC-2000; 2000US-235281P.
XX
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
XX Schlegel R, Endege WO, Monahan JE;
XX
XX WPI; 2001-662795/76.
XX
XX Novel isolated nucleic acid molecule associated with cancerous state of
XX prostate cells and correlating with presence of prostate cancer, useful
XX for detecting presence of prostate cancer, stage of prostate cancer -
XX
XX Claim 1; Page 3912; 11750pp; English.
XX
XX The invention relates to an isolated nucleic acid molecule (I) comprising
XX a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
XX specification or its complement. (I) is useful for:
```

CC (a) assessing whether a patient is afflicted with prostate cancer;
CC (b) monitoring the progression of prostate cancer in a patient;
CC (c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;
CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound;
CC (g) determining whether prostate cancer has metastasized in a patient;
CC (h) assessing the aggressiveness or indolence of prostate cancer in a patient;
CC (i) is also useful as a pharmacodynamic or pharmacogenomic marker.

Sequence 1194 BP; 288 A; 287 C; 278 G; 339 T; 2 other;

Alignment Scores:

Pred. No.:	1,05e-142	Length:	1194
Score:	150.00	Matches:	150
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	78.95%	Indels:	0
DB:	23	Gaps:	0

US-09-895-298a-83 (1-190) x ABV22463 (1-1194)

QY 1 MetMetAsnPhgInPrProSerLysAlaTrpArgAlaSerGlnMetMetTrhPhePhe 20
|||||
DB 531 ATGATGAAATTTCCAGCTCCGAGCAAGCCTGGCGGCTCACAGATGATGACTTTCTTC 590
QY 21 IlePheLeuPhePheProSerPheTrhGlyValLeuGlySerTrhLeuAlaIleTrhIle 40
|||||
DB 591 ATCTTGTGCTTTTCCATCCCTTCCACCGGGGCTTGTGACCCCTGGCCATCACCATC 650
QY 41 TrpArgLeuLysProSerAlaAspCysGlyProPheArgGlyLeuProLeuPheIleHis 60
|||||
DB 651 TGGAGATTGAAGCTTACGACTGTGGCCCTTTTGAGGTCTGCTCTCTTCATTTCAC 710
QY 61 SerIleTrpSerTrpIleAspTrhLeuSerTrhArgProGlyTrpValIleValTrp 80
|||||
DB 711 TCCATCTACAGCTGTGATGACACCCCTTCAAGTACACGGCCCTGGCTGTGTTGG 770
QY 81 IleTrpArgAsnLeuIleGlySerValHisPhePheIleLeuTrhIleValLeu 100
|||||
DB 771 ATCATGGAACCTCATTTGGAAGTGTGACTCTTTTTCATCTCCACCTCATTTGCTCA 830
QY 101 IleIleTrhTrpLeuTrpTrpGlnIleTrhGlyValArgLysIleMetIleArgLeuLeu 120
|||||
DB 831 ATCATGCACTATCTTACTGGCAGATCACAGAGGAAGAAATTAATGATAGGCTCTC 890
QY 121 HisGlnGlnIleIleAsnGlyLysAspLysMetPheLeuIleGlyLysLeuIleLys 140
|||||
DB 891 CATGAGCAGATCATTAATGAGGCAAGATAAATGTTCTTGATAGAAAATGATCAAG 950
QY 141 LeuGlnAspMetGlyLysLysAlaAsnPro 150
DB 951 CTGAGGATATGAGAAAGAAACCA 980

RESULT 12
ABV25683
ID ABV25683 standard; cDNA; 1194 BP.
AC ABV25683;
XX
DT 16-SEP-2002 (first entry)
XX
DE Human prostate expression marker cDNA 25674.
XX
KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
XX pharmacogenomic marker; gene; ss.
XX
OS Homo sapiens.
XX
PN W0200160860-A2.

XX 23-AUG-2001.
PD
XX
PF 20-FEB-2001; 2001MO-US05171.
XX
PR 17-FEB-2000; 2000US-183319P.
PR 16-MAR-2000; 2000US-189862P.
PR 25-MAY-2000; 2000US-207454P.
PR 09-JUN-2000; 2000US-211314P.
PR 18-JUL-2000; 2000US-219007P.
PR 13-DEC-2000; 2000US-255281P.
XX
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI Schlegel R, Endege WO, Monahan JE;
XX
DR WPI; 2001-662795/76.
XX
DR
XX
PT Novel isolated nucleic acid molecule associated with cancerous state of
PT prostate cells and correlating with presence of prostate cancer, useful
PT for detecting presence of prostate cancer, stage of prostate cancer -
XX
XX
PS Claim 1; Page 5146-5147; 11750pp; English.

CC The invention relates to an isolated nucleic acid molecule (I) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement. (I) is useful for:
CC (a) assessing whether a patient is afflicted with prostate cancer;
CC (b) monitoring the progression of prostate cancer in a patient;
CC (c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;
CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound;
CC (g) determining whether prostate cancer has metastasized in a patient;
CC (h) assessing the aggressiveness or indolence of prostate cancer in a patient;
CC (i) is also useful as a pharmacodynamic or pharmacogenomic marker.

Sequence 1194 BP; 288 A; 287 C; 278 G; 339 T; 2 other;

Alignment Scores:

Pred. No.:	1,05e-142	Length:	1194
Score:	150.00	Matches:	150
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	78.95%	Indels:	0
DB:	23	Gaps:	0

US-09-895-298a-83 (1-190) x ABV25683 (1-1194)

QY 1 MetMetAsnPhgInPrProSerLysAlaTrpArgAlaSerGlnMetMetTrhPhePhe 20
|||||
DB 531 ATGATGAAATTTCCAGCTCCGAGCAAGCCTGGCGGCTCACAGATGATGACTTTCTTC 590
QY 21 IlePheLeuPhePheProSerPheTrhGlyValLeuGlySerTrhLeuAlaIleTrhIle 40
|||||
DB 591 ATCTTGTGCTTTTCCATCCCTTCCACCGGGGCTTGTGACCCCTGGCCATCACCATC 650
QY 41 TrpArgLeuLysProSerAlaAspCysGlyProPheArgGlyLeuProLeuPheIleHis 60
|||||
DB 651 TGGAGATTGAAGCTTACGACTGTGGCCCTTTTGAGGTCTGCTCTCTTCATTTCAC 710
QY 61 SerIleTrpSerTrpIleAspTrhLeuSerTrhArgProGlyTrpValIleValTrp 80
|||||
DB 711 TCCATCTACAGCTGTGATGACACCCCTTCAAGTACACGGCCCTGGCTGTGTTGG 770
QY 81 IleTrpArgAsnLeuIleGlySerValHisPhePheIleLeuTrhIleValLeu 100
|||||
DB 771 ATCATGGAACCTCATTTGGAAGTGTGACTCTTTTTCATCTCCACCTCATTTGCTCA 830
QY 101 IleIleTrhTrpLeuTrpTrpGlnIleTrhGlyValArgLysIleMetIleArgLeuLeu 120

|||||
Db 831 ATCATCACCCTATCTTACTGCGAGATCACAGGAGGAGAGATATGATAGCGCTGTC 890
Qy 121 HtSGlUGlnIlelleasnglUlysAspLysMetPheLeuIlGluLysLeuIleLys 140
Db 891 CATGAGCAGATCATTTAATGACGAGCAAGATTAATAATGTTCTGATGAAAAATTGATCAAG 950
Qy 141 LeuGlnAspMetGluLysLysAlaAsnPro 150
Db 951 CTGCAGATATGTGAGAGAAAGCAAAACCA 980
RESULT 13
ABV28278
ID ABV28278 standard; cDNA; 1194 BP.
XX AC ABV28278;
XX DT 16-SEP-2002 (first entry)
XX DE Human prostate expression marker cDNA 28269.
XX KM Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
XX KW Pharmacogenomic marker; gene; ss.
XX OS Homo sapiens.
XX PN WO200160860-A2.
XX PD 23-AUG-2001.
XX PF 20-FEB-2001; 2001WO-US05171.
XX PR 17-FEB-2000; 2000US-183319P.
XX PR 16-MAR-2000; 2000US-189862P.
XX PR 25-MAY-2000; 2000US-207454P.
XX PR 09-JUN-2000; 2000US-211314P.
XX PR 18-JUL-2000; 2000US-219007P.
XX PR 13-DEC-2000; 2000US-255281P.
XX PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX PI Schlegel R, Endege WO, Monahan JE;
XX DR WPI; 2001-662795/76.
XX XX
XX PT Novel isolated nucleic acid molecule associated with cancerous state of
XX PT prostate cells and correlating with presence of prostate cancer, useful
XX PT for detecting presence of prostate cancer, stage of prostate cancer -
XX PS Claim 1; Page 5881-5882; 11750pp; English.
XX XX
XX CC The invention relates to an isolated nucleic acid molecule (I) comprising
XX CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
XX CC specification or its complement. (I) is useful for:
XX CC (a) assessing whether a patient is afflicted with prostate cancer;
XX CC (b) monitoring the progression of prostate cancer in a patient;
XX CC (c) assessing the efficacy of a test compound to inhibit prostate
XX CC cancer in a patient;
XX CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
XX CC in a patient;
XX CC (e) selecting a composition for inhibiting prostate cancer in a patient;
XX CC (f) assessing the prostate cell carcinogenic potential of a compound;
XX CC (g) determining whether prostate cancer has metastasized in a patient;
XX CC (h) assessing the aggressiveness or indolence of prostate cancer in a
XX CC patient;
XX CC (I) is also useful as a pharmacodynamic or pharmacogenomic marker.
XX SQ Sequence 1194 BP; 288 A; 287 C; 278 G; 339 T; 2 other:
Alignment Scores:
Pred. No.: 1.05e-142 Length: 1194
Score: 150.00 Matches: 150
Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0
Query Match: 78.95% Indels: 0
DB: 23 Gaps: 0
US-09-895-298a-83 (1-190) x ABV28278 (1-1194)
Qy 1 MetMetAsnPhgInProProSerLysAlaTrpAlaGlaserGlnMetMetThrPhePhe 20
Db 531 ATGATGATTTTCCACGCTCCGAGCAAGCCTGGGGGCTCCACATATGATGATCTTCTTC 590
Qy 21 IlePheLeuLeuPhePheProSerPheThrGlyValLeuCysThrLeuAlaIleThrIle 40
Db 591 ATCTTCTGCTCTTTTCCATCCTTCACCGGGGCTCTGTGCACCTGGCCATCACATTC 650
Qy 41 TrpArgLeuLysProSerAlaAspCysGlyProPheArgGlyLeuProLeuPheIleHis 60
Db 651 TGGAGATTGAAGCCTTCAGCTGAGCTGGCCCTTTTCGAGGCTGCTCTTCAATTCAC 710
Qy 61 SerIleTySerTrpIleAspThrLeuSerThrArgProGlyTyLeuTrpValAlaTrp 80
Db 711 TCCATCTACAGCTGGATGACACCCCTAGTACAGCGCTGCTGCTGTGGTGTGG 770
Qy 81 IleTyArgAsnLeuIleGlySerValHisPhePheIleLeuThrLeuIleValLeu 100
Db 771 ATCTATCGGAACTCATTTGGAAGTGTGCACCTTTTTCATCTCACCCTCATTTGTGCTA 830
Qy 101 IleIleThrTyLeuTyTrpGlnIleThrGlnGlyArgGlyIleMetIleArgLeuLeu 120
Db 831 ATCATCACCCTATCTTACTGCGAGATCACAGAGGAGGAGAGATTAATGATTAAGCTGCTC 890
Qy 121 HtSGlUGlnIlelleasnglUlysAspLysMetPheLeuIlGluLysLeuIleLys 140
Db 891 CATGAGCAGATCATTTAATGACGAGCAAGATTAATAATGTTCTGATGAAAAATTGATCAAG 950
Qy 141 LeuGlnAspMetGluLysLysAlaAsnPro 150
Db 951 CTGCAGATATGTGAGAGAAAGCAAAACCA 980
RESULT 14
AAL18591
ID AAL18591 standard; cDNA; 470 BP.
XX AC AAL18591;
XX AC AAL18591;
XX DT 07-DEC-2001 (first entry)
XX DE Human breast cancer expressed polynucleotide 11048.
XX DE Human; breast cancer; cell marker; cytostatic; ss.
XX KW
XX OS Homo sapiens.
XX XX
XX PN WO200151628-A2.
XX PD 19-JUL-2001.
XX PF 10-JAN-2001; 2001WO-US00798.
XX PR 14-JAN-2000; 2000US-0176077.
XX PR 14-MAR-2000; 2000US-0189167.
XX PR 24-MAR-2000; 2000US-0192099.
XX PR 29-MAR-2000; 2000US-0193480.
XX PR 15-MAY-2000; 2000US-0205230.
XX PR 09-JUN-2000; 2000US-0211315.
XX PR 25-JUL-2000; 2000US-0220534.
XX PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX PI Lillie J, Xu Y, Wang Y, Steinmann K;
XX DR WPI; 2001-451856/48.
XX PT New peptide useful as a marker for the diagnosis of breast cancer -

XX Claim 1; Page 1968; 3695pp; English.
XX
CC The invention relates to human breast cancer expressed polynucleotides
CC (AA07544-AL26789) and methods of assessing whether a patient is
CC afflicted with breast cancer by examining the correlation between the
CC expression of certain markers and the cancerous state of breast cells.
CC The polynucleotides and encoded polypeptides are potential markers for
CC detecting, diagnosing, monitoring, characterizing treating and
CC potentially preventing breast cancer. The polynucleotides and encoded
CC polypeptides are also useful for isolating compounds with cytostatic
CC activity.
XX
SQ Sequence 470 BP; 144 A; 92 C; 116 G; 118 T; 0 other;
XX
Alignment Scores:
Pred. No.: 1,32e-112 Length: 470
Score: 120.00 Matches: 120
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 63.16% Indels: 0
DB: Gaps: 0
US-09-895-298a-83 (1-190) x AAL18591 (1-470)
QY 71 ThrArgProGlyTyrLeuTrpValValTrpIleTyrArgAsnLeuIleGlySerValHis 90
DB 5 ACAGGGCCCTGGCTACCTGTGGGTGTGGATCTATCGAACCCTCATTTGGAAAGTGTGCAC 64
QY 91 PhePhePheIleuTrpIleuValLeuIleIleThrTyrLeuTyrTrpGlnIleThr 110
DB 65 TTTCTTTTCACTCCACCTCATTTGTCTATATCATCACTTACTTCTTCTGCGACATCACA 124
QY 111 GluGlyArgLysIleMetIleArgLeuLeuHisGluGlnIleIleAsnGluGlyLysASP 130
DB 125 GAGGGAAGAAGATTATGATTAAGGCTCTCCATGACAGATCATTAATGAGGCAAAAGAT 184
QY 131 LysMetPheLeuIleGluLysLeuIleLysLeuGlnAspMetGluLysLysAlaAsnPro 150
DB 185 AAAATGTTCTGTAGTAAATAATGATCATCACTGATGAGATATGAGAAAGCAAAACCCC 244
QY 151 SerSerLeuValLeuGluArgArgGluValGluGlnGlnIlePheLeuHisLeuGlyGlu 170
DB 245 AGCTCACTTTGTTCTGGAAAGAGAGAGGTGAGCACAAGGCTTTTGGATTGGGGAA 304
QY 171 HisAspLysSerLeuAspLeuArgSerArgArgSerValGlnGluLysAsnProArgAla 190
DB 305 CATGATGCGAGTCTTGACTTGGCATCTAGAAAGATCACTTCAAGAGAGTATCCAAAGGCC 364
RESULT 15
AAL09919
ID AAL09919 standard; cDNA; 501 BP.
XX
AC AAL09919;
XX
DT 07-DEC-2001 (first entry)
XX
DE Human breast cancer expressed polynucleotide 2376.
XX
KM Human; breast cancer; cell marker; cytostatic; ss.
XX
OS Homo sapiens.
XX
PN WO200151628-A2.
XX
PD 19-JUL-2001.
XX
PE 10-JAN-2001; 2001MO-US00798.
XX
PR 14-JAN-2000; 2000US-0176077.
PR 14-MAR-2000; 2000US-0189167.
PR 24-MAR-2000; 2000US-0192099.
PR 29-MAR-2000; 2000US-0193480.

PR 15-MAY-2000; 2000US-0205230.
PR 09-JUN-2000; 2000US-0211315.
PR 25-JUN-2000; 2000US-0220534.
XX
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI Little J, Xu Y, Wang Y, Steilmann K;
XX
DR WPI; 2001-451856/48.
XX
PT New peptide useful as a marker for the diagnosis of breast cancer -
XX
PS Claim 1; Page 455; 3695pp; English.
XX
SQ Sequence 501 BP; 147 A; 101 C; 128 G; 122 T; 3 other;
XX
Alignment Scores:
Pred. No.: 2,04e-102 Length: 501
Score: 110.00 Matches: 110
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 57.89% Indels: 0
DB: Gaps: 0
US-09-895-298a-83 (1-190) x AAL09919 (1-501)
QY 71 ThrArgProGlyTyrLeuTrpValValTrpIleTyrArgAsnLeuIleGlySerValHis 90
DB 36 ACAGGGCCCTGGCTACCTGTGGGTGTGGATCTATCGAACCCTCATTTGGAAAGTGTGCAC 95
QY 91 PhePhePheIleuTrpIleuValLeuIleIleThrTyrLeuTyrTrpGlnIleThr 110
DB 96 TTTCTTTTCACTCCACCTCATTTGTCTATATCATCACTTACTTCTTCTGCGACATCACA 155
QY 111 GluGlyArgLysIleMetIleArgLeuLeuHisGluGlnIleIleAsnGluGlyLysASP 130
DB 156 GAGGGAAGAAGATTATGATTAAGGCTCTCCATGACAGATCATTAATGAGGCAAAAGAT 215
QY 131 LysMetPheLeuIleGluLysLeuIleLysLeuGlnAspMetGluLysLysAlaAsnPro 150
DB 216 AAAATGTTCTGTAGTAAATAATGATCATCACTGATGAGATATGAGAAAGCAAAACCCC 275
QY 151 SerSerLeuValLeuGluArgArgGluValGluGlnGlnIlePheLeuHisLeuGlyGlu 170
DB 276 AGCTCACTTTGTTCTGGAAAGAGAGAGGTGAGCACAAGGCTTTTGGATTGGGGAA 335
QY 171 HisAspLysSerLeuAspLeuArgSerArg 180
DB 336 CATGATGCGAGTCTTGACTTGGCATCTAGAA 365

Search completed: November 9, 2002, 07:45:52
Job time : 305 secs